



## SEQUENCE LISTING

&lt;110&gt; M&amp;E Biotech A/S

&lt;120&gt; Method for down-regulating GDF-8 activity

&lt;130&gt; AutoVacGDF-8 DK 1

&lt;160&gt; 23

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile  
1 5 10 15

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
35 40 45

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu  
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
115 120 125

Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160

Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
 210 215 220  
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
 225 230 235 240  
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys  
 245 250 255  
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
 260 265 270  
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
 275 280 285  
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300  
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
 340 345 350  
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
 355 360 365  
 Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 2  
 <211> 362  
 <212> PRT  
 <213> Meleagris gallopavo

<400> 2  
 Met Gln Ile Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro  
 1 5 10 15  
 Thr Glu Asn Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg  
 20 25 30  
 Gln Asn Thr Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu  
 35 40 45  
 Ser Lys Leu Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile  
 50 55 60  
 Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln  
 65 70 75 80  
 Tyr Asp Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp

85	90	95
Asp Tyr His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser 100	105	110
Asp Phe Leu Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys 115	120	125
Phe Ser Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp 130	135	140
Ile Tyr Leu Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile 145	150	155
Leu Arg Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile 165	170	175
Arg Ser Leu Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser 180	185	190
Ile Asp Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser 195	200	205
Asn Leu Gly Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu 210	215	220
Ala Val Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu 225	230	235
Glu Val Arg Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly 245	250	255
Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro 260	265	270
Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro 275	280	285
Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe 290	295	300
Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg 305	310	315
Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn 325	330	335
Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro 340	345	350
Ala Met Val Val Asp Arg Cys Gly Cys Ser 355	360	

<210> 3  
 <211> 375  
 <212> PRT

<213> Gallus sp.

<400> 3

Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile  
1 5 10 15  
Ala Val Asp Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn  
20 25 30  
Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
35 40 45  
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
50 55 60  
Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu  
65 70 75 80  
Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95  
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110  
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
115 120 125  
Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140  
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160  
Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175  
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190  
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
195 200 205  
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
210 215 220  
Ile Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr  
225 230 235 240  
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg  
245 250 255  
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
260 265 270  
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
275 280 285

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
290 295 300

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
355 360 365

Val Asp Arg Cys Gly Cys Ser  
370 375

<210> 4  
<211> 376  
<212> PRT  
<213> Mus musculus

<400> 4

Met Met Gln Lys Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu  
1 5 10 15

Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu  
20 25 30

Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn  
35 40 45

Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys  
50 55 60

Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln  
65 70 75 80

Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp  
85 90 95

Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr  
100 105 110

His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe  
115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
130 135 140

Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
145 150 155 160

Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg  
165 170 175

Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser  
 180 185 190  
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
 195 200 205  
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
 210 215 220  
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
 225 230 235 240  
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
 245 250 255  
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
 260 265 270  
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 275 280 285  
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
 290 295 300  
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
 305 310 315 320  
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
 325 330 335  
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
 340 345 350  
 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met  
 355 360 365  
 Val Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 5  
 <211> 375  
 <212> PRT  
 <213> Bos taurus

<400> 5  
 Met Gln Lys Leu Gln Ile Ser Val Tyr Ile Tyr Leu Phe Met Leu Ile  
 1 5 10 15  
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
 20 25 30  
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr  
 35 40 45  
 Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu

50	55	60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu		
65	70	75 80
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val		
	85	90 95
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His		
	100	105 110
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu		
	115	120 125
Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser		
	130	135 140
Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu		
	145	150 155 160
Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu		
	165	170 175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu		
	180	185 190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val		
	195	200 205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly		
	210	215 220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr		
	225	230 235 240
Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys		
	245	250 255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys		
	260	265 270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val		
	275	280 285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr		
	290	295 300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys		
	305	310 315 320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala		
	325	330 335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr		
	340	345 350
Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val		

355	360	365
Val Asp Arg Cys Gly Cys Ser		
370	375	
<210> 6		
<211> 375		
<212> PRT		
<213> Ovis sp.		
<400> 6		
Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu		
1	5	10 15
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn		
	20	25 30
Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn		
	35	40 45
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu		
	50	55 60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu		
	65	70 75 80
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val		
	85	90 95
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His		
	100	105 110
Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu		
	115	120 125
Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser		
	130	135 140
Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu		
145	150	155 160
Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu		
	165	170 175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu		
	180	185 190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val		
	195	200 205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly		
	210	215 220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr		
225	230	235 240



His Ala Thr Thr Glu Thr Ile Ile Thr Met'Pro Thr Glu Ser Asp Phe  
115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
 130 135 140  
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
 145 150 155 160  
 Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg  
 165 170 175  
 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser  
 180 185 190  
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
 195 200 205  
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
 210 215 220  
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
 225 230 235 240  
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
 245 250 255  
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
 260 265 270  
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 275 280 285  
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
 290 295 300  
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
 305 310 315 320  
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
 325 330 335  
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
 340 345 350  
 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met  
 355 360 365  
 Val Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 8  
 <211> 375  
 <212> PRT  
 <213> Sus scrofa

<400> 8  
 Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile

1	5	10	15
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn	20	25	30
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr	35	40	45
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	50	55	60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu	65	70	75
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val	85	90	95
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	100	105	110
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu	115	120	125
Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	130	135	140
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu	145	150	155
Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu	165	170	175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	180	185	190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	195	200	205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	210	215	220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr	225	230	235
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys	245	250	255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	260	265	270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	275	280	285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	290	295	300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys			

305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
355 360 365

Val Asp Arg Cys Gly Cys Ser  
370 375

<210> 9  
<211> 374  
<212> PRT  
<213> Danio rerio

<400> 9

Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys  
1 5 10 15

Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr  
20 25 30

Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His  
35 40 45

Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys  
50 55 60

Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln  
65 70 75 80

Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp  
85 90 95

Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu  
100 105 110

His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro  
115 120 125

Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser  
130 135 140

Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His  
145 150 155 160

Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg  
165 170 175

Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys  
180 185 190

Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys  
 195 200 205  
 Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile  
 210 215 220  
 Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser  
 225 230 235 240  
 Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile  
 245 250 255  
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp  
 260 265 270  
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp  
 275 280 285  
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys  
 290 295 300  
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr  
 305 310 315 320  
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly  
 325 330 335  
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe  
 340 345 350  
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val  
 355 360 365  
 Asp Arg Cys Gly Cys Ser  
 370

<210> 10  
 <211> 375  
 <212> PRT  
 <213> Papio hamadryas

<400> 10  
 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile  
 1 5 10 15  
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
 20 25 30  
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
 35 40 45  
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
 50 55 60  
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
 65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
115 120 125

Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
145 150 155 160

Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
225 230 235 240

Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys  
245 250 255

Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
260 265 270

Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
275 280 285

Asp Phe Glu Ala Leu Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
290 295 300

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
305 310 315 320

Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
325 330 335

Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
340 345 350

Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
355 360 365

Val Asp Arg Cys Gly Cys Ser  
370 375

<210> 11  
<211> 109  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)..(109)  
<223> Identical to residues 267-375 in SEQ ID NO: 1

<400> 11  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15  
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30  
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45  
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60  
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80  
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95  
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 12  
<211> 109  
<212> PRT  
<213> Bos taurus

<220>  
<221> PEPTIDE  
<222> (1)..(109)  
<223> Identical to residues 267-375 in SEQ ID NO: 5

<400> 12  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15  
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30  
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45  
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly  
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 13  
<211> 15  
<212> PRT  
<213> Clostridium tetani

<400> 13  
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

<210> 14  
<211> 21  
<212> PRT  
<213> Clostridium tetani

<400> 14  
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15

Ala Ser His Leu Glu  
20

<210> 15  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (18)..(32)  
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
<221> SIMILAR  
<222> (1)..(17)  
<223> Identical to residues 267-283 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (33)..(109)  
<223> Identical to residues 299-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser



<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<400> 15  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15  
Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
20 25 30  
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45  
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60  
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80  
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95  
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 16  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (52)..(66)  
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
<221> SIMILAR  
<222> (1)..(51)  
<223> Identical to residues 267-317 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (67)..(109)  
<223> Identical to residues 333-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser

<220>  
<221> SITE  
<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 16

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr  
50 55 60

Glu Leu Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 17

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (83)..(97)

<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>

<221> SIMILAR

<222> (1)..(82)

<223> Identical to residues 267-348 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (98)..(109)

<223> Identical to residues 364-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 17

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys

1	5	10	15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile			
20	25	30	
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu			
35	40	45	
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala			
50	55	60	
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser			
65	70	75	80
Pro Ile Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu			
85	90	95	
Leu Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser			
100	105		

<210> 18  
 <211> 109  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (21)..(41)  
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> SIMILAR  
 <222> (42)..(109)  
 <223> Identical to residues 307-375 in SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (42)..(109)  
 <223> Identical to residues 308-375 in SEQ ID NO: 1

<220>  
 <221> SITE  
 <222> (73)  
 <223> Cys or Ser

<220>  
 <221> SITE  
 <222> (90)..(91)  
 <223> Lys Glu or Glu Gly

<400> 18
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
20 25 30



Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
50 55 60

Ala Ser His Leu Glu Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80  
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly  
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 20  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (79)..(99)  
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> SIMILAR  
<222> (1)..(78)  
<223> Identical to residues 267-345 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (100)..(109)  
<223> Identical to residues 366-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser

<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<400> 20  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Phe Asn  
65 70 75 80

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser  
85 90 95

His Leu Glu Ala Met Val Val Asp Arg Cys Gly Cys Ser  
100 105

<210> 21  
<211> 109  
<212> PRT  
<213> Artificial sequence

<220>  
<221> MUTAGEN  
<222> (84)..(104)  
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> SIMILAR  
<222> (1)..(83)  
<223> Identical to residues 267-349 in SEQ ID NO: 1

<220>  
<221> SIMILAR  
<222> (105)..(109)  
<223> Identical to residues 371-375 in SEQ ID NO: 1

<220>  
<221> SITE  
<222> (73)  
<223> Cys or Ser

<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<400> 21  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro Ile Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro  
85 90 95

Lys Val Ser Ala Ser His Leu Glu Arg Cys Gly Cys Ser  
100 105

<210> 22  
<211> 254  
<212> PRT  
<213> Artificial sequence

<220>  
<221> SIMILAR  
<222> (110)..(124)  
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
<221> SIMILAR  
<222> (125)..(145)  
<223> Diphtheria toxoid P30 epitope (SEQ ID NO: 14)

<220>  
<221> SIMILAR  
<222> (1)..(109)  
<223> 109 C-terminal residues of human and bovine GDF-8  
(residues 267-375 in SEQ ID NO: 1)

<220>  
<221> SIMILAR  
<222> (146)..(254)  
<223> 109 C-terminal residues of human and bovine GDF-8  
(residues 267-375 in SEQ ID NO: 1)

<220>  
<221> SITE  
<222> (90)..(91)  
<223> Lys Glu or Glu Gly

<220>  
<221> SITE  
<222> (235)..(236)  
<223> Identical to (90)..(91)

<400> 22  
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys  
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile  
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala  
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
65 70 75 80

Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly			
				85					90					95				
Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser	Gln	Tyr	Ile			
			100					105					110					
Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Leu	Phe	Asn	Asn	Phe			
		115					120					125						
Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu			
	130					135					140							
Glu	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys			
145					150				155						160			
Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp			
			165					170						175				
Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys			
		180						185					190					
Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln			
	195					200						205						
Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met			
	210					215					220							
Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr			
225				230					235						240			
Gly	Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser					
			245					250										

<210> 23  
 <211> 160  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> MUTAGEN  
 <222> (16)..(36)  
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>  
 <221> MUTAGEN  
 <222> (37)..(51)  
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>  
 <221> SIMILAR  
 <222> (1)..(15)  
 <223> Identical to residues 216-230 of SEQ ID NO: 1

<220>  
 <221> SIMILAR  
 <222> (52)..(160)



<223> Identical to residues 267-375 of SEQ ID NO: 1

<220>

<221> SITE

<222> (124)

<223> Cys or Ser

<220>

<221> SITE

<222> (141)..(142)

<223> Lys Glu or Glu Gly

<400> 23

Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile Lys Ala Leu Phe  
1 5 10 15

Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala  
20 25 30

Ser His Leu Glu Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile  
35 40 45

Thr Glu Leu Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser  
50 55 60

Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp  
65 70 75 80

Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly  
85 90 95

Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val  
100 105 110

His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr  
115 120 125

Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile  
130 135 140

Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser  
145 150 155 160

<210> 24

<211> 13

<212> PRT

<213> Unknown

<400> 24

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala  
1 5 10 15